

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 346.117 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-1

Perfect score: 18

Sequence: 1 cgcaagctgaaaaagtag 18

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
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15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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24:	/cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
25:	/cgn2_6/ptodata/2/pubpna/US11B_PUBCOMB.seq.*
26:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
27:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
28:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	US-10-025-137-1	Sequence 1, Appli
2	18	100.0	24	US-10-025-137-3	Sequence 3, Appli
C 3	16.4	91.1	233	21 US-10-425-115-157137	Sequence 157137,
4	16.4	91.1	700	14 US-10-027-632-149388	Sequence 149388,
5	16.4	91.1	700	18 US-10-027-632-149388	Sequence 149388,

6	16.4	91.1	2310	18	US-10-369-493-46035	Sequence 46035, A
7	16.4	91.1	2490	9	US-09-974-300-4328	Sequence 4328, Ap
8	16.4	91.1	3490	24	US-10-510-408-48	Sequence 48, Appl
9	16	88.9	351	20	US-10-430-201-2755	Sequence 2755, Ap
10	16	88.9	351	20	US-10-430-201-2756	Sequence 2756, Ap
11	16	88.9	1592	21	US-10-723-860-2804	Sequence 2804, Ap
12	16	88.9	1834	21	US-10-723-860-6882	Sequence 6882, Ap
C 13	16	88.9	2940	10	US-09-814-353-21490	Sequence 21490, A
14	15.4	85.6	393	22	US-10-472-928-1003	Sequence 1003, Ap
15	15.4	85.6	488	10	US-09-770-961-739	Sequence 739, App
C 16	15.4	85.6	493	13	US-09-925-065A-747566	Sequence 747566,
C 17	15.4	85.6	493	13	US-09-925-065A-747567	Sequence 747567,
C 18	15.4	85.6	493	13	US-09-925-065A-747568	Sequence 747568,
19	15.4	85.6	555	18	US-10-282-122A-27952	Sequence 27952, A
20	15.4	85.6	589	13	US-09-925-065A-619093	Sequence 619093,
21	15.4	85.6	612	13	US-09-925-065A-731537	Sequence 731537,
22	15.4	85.6	612	13	US-09-925-065A-731538	Sequence 731538,
C 23	15.4	85.6	653	13	US-09-925-065A-274420	Sequence 274420,
C 24	15.4	85.6	653	13	US-09-925-065A-274421	Sequence 274421,
C 25	15.4	85.6	653	13	US-09-925-065A-274422	Sequence 274422,
C 26	15.4	85.6	963	19	US-10-424-599-50975	Sequence 50975, A
C 27	15.4	85.6	1200	21	US-10-739-930-3873	Sequence 3873, Ap
C 28	15.4	85.6	1221	18	US-10-369-493-43501	Sequence 43501, A
C 29	15.4	85.6	1260	13	US-09-925-065A-674296	Sequence 674296,
30	15.4	85.6	1503	9	US-09-974-300-481	Sequence 481, App
31	15.4	85.6	1539	9	US-09-974-300-493	Sequence 493, App
32	15.4	85.6	2658	18	US-10-282-122A-26897	Sequence 26897, A
33	15.4	85.6	11378	8	US-08-961-527-210	Sequence 210, App
34	15.4	85.6	11378	18	US-10-158-844-210	Sequence 210, App
35	15.4	85.6	92407	19	US-10-672-787-36	Sequence 16, Appl
C 36	15.4	85.6	203264	14	US-10-087-192-988	Sequence 988, App
37	15.4	85.6	253861	20	US-10-741-601-5611	Sequence 5611, Ap
38	15.4	85.6	261817	14	US-10-087-192-2002	Sequence 2002, Ap
39	15.4	85.6	385320	22	US-10-741-600-17796	Sequence 17796, A
40	15.4	85.6	2162598	22	US-10-472-928-4979	Sequence 4979, Ap
C 41	15	83.3	25	22	US-10-719-900-310367	Sequence 310367,
C 42	15	83.3	25	22	US-10-719-900-364148	Sequence 364148,
C 43	15	83.3	25	22	US-10-719-900-560295	Sequence 560295,
C 44	15	83.3	25	22	US-10-719-900-610415	Sequence 610415,
C 45	15	83.3	25	22	US-10-719-900-618457	Sequence 618457,

ALIGNMENTS

RESULT 1
US-10-025-137-1
; Sequence 1, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Terng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025, 137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-10-025-137-1

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy . 1 CGCAAGCTGAAAAAGTAG 18
|||||

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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 46.7435 seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-1

Perfect score: 18

Sequence: 1 CGCAAGCTGAAAGTAG 18

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgm2_6/ptodata/1/ina/5A_COMB.seq.*
- 2: /cgm2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgm2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgm2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgm2_6/ptodata/1/ina/PCTUS_COMB.seq.*
- 6: /cgm2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	16.4	91.1	24280	4	US-09-949-016-15622, A
C 3	15.4	85.6	396	4	US-09-583-110-234, A
C 4	15.4	85.6	601	4	US-09-949-016-76457, A
C 5	15.4	85.6	601	4	US-09-949-016-76458, A
C 6	15.4	85.6	999	4	US-09-902-540-8492, A
C 7	15.4	85.6	1914	4	US-09-540-236-1278, A
C 8	15.4	85.6	2256	4	US-09-540-236-400, A
C 9	15.4	85.6	7538	4	US-09-902-540-894, A
C 10	15.4	85.6	11378	3	US-08-961-527-210, A
C 11	15.4	85.6	31861	4	US-09-949-016-12803, A
C 12	15.4	85.6	31861	4	US-09-949-016-13967, A
C 13	15.4	85.6	92407	4	US-09-586-002-36, A
C 14	15.4	85.6	141248	4	US-09-949-016-12241, A
C 15	15.4	85.6	143248	4	US-09-949-016-16652, A
C 16	15.4	85.6	194937	4	US-09-949-016-17032, A
C 17	15.4	85.6	194937	4	US-09-949-016-17033, A
C 18	15.4	85.6	200663	4	US-09-949-016-12569, A
C 19	15.4	85.6	203093	4	US-09-949-016-14445, A
C 20	15.4	85.6	818128	4	US-09-949-016-14547, A
C 21	15.4	85.6	818128	4	US-09-949-016-14548, A
C 22	15.4	85.6	818128	4	US-09-949-016-14549, A
C 23	15.4	85.6	818128	4	US-09-949-016-14550, A
C 24	15.4	85.6	818128	4	US-09-949-016-14551, A
C 25	15.4	85.6	818128	4	US-09-949-016-14552, A
C 26	15.4	85.6	818128	4	US-09-949-016-14553, A
C 27	15.4	85.6	818128	4	US-09-949-016-14554, A

28	15.4	85.6	818128	4	US-09-949-016-14554, A
29	15.4	85.6	818128	4	US-09-949-016-14555, A
30	15.4	85.6	818128	4	US-09-949-016-14556, A
31	15.4	85.6	818128	4	US-09-949-016-14557, A
32	15.4	85.6	818128	4	US-09-949-016-14558, A
33	15.4	85.6	818128	4	US-09-949-016-14559, A
34	15.4	85.6	818128	4	US-09-949-016-14560, A
35	15.4	85.6	818128	4	US-09-949-016-14561, A
36	15.4	85.6	818128	4	US-09-949-016-14562, A
37	15.4	85.6	818128	4	US-09-949-016-14563, A
38	15.4	85.6	818128	4	US-09-949-016-14564, A
39	15.4	85.6	818128	4	US-09-949-016-14565, A
40	15.4	85.6	818128	4	US-09-949-016-14566, A
C 41	15	83.3	601	4	US-09-949-016-38946, A
C 42	15	83.3	601	4	US-09-949-016-38947, A
C 43	15	83.3	601	4	US-09-949-016-38948, A
C 44	15	83.3	601	4	US-09-949-016-38949, A
C 45	15	83.3	601	4	US-09-949-016-128437, A

ALIGNMENTS

RESULT 1
US-09-949-016-15621/c
; Sequence 15621, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15621
; LENGTH: 24280
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15621

Query Match 91.1%; Score 16.4; DB 4; Length 24280;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCAAGCTGAAAGTAG 18
DB 18059 CGCAAGCTGAAAGTAG 18042

RESULT 2
US-09-949-016-15622/c
; Sequence 15622, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 499.99 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-8

Perfect score: 26

Sequence: 1 gttatgtattgctgttgcggcg 26

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*

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22: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*

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28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	18.8	72.3	765	20	Sequence 8, Appl1
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4	18.8	72.3	914	18	Sequence 325205,
5	18.6	71.5	507	19	Sequence 325205,
					Sequence 106771,

c 6	18.6	71.5	516	13	US-09-925-065A-284063	Sequence 284063,
c 7	18.6	71.5	516	13	US-09-925-065A-284064	Sequence 284064,
c 8	18.6	71.5	538	13	US-09-925-065A-586080	Sequence 586080,
9	18.6	71.5	538	13	US-09-925-065A-586081	Sequence 586081,
10	18.6	71.5	538	13	US-09-925-065A-586082	Sequence 586082,
11	18.6	71.5	591	13	US-09-925-065A-636500	Sequence 636500,
c 12	18.6	71.5	612	13	US-09-925-065A-377541	Sequence 377541,
c 13	18.6	71.5	612	13	US-09-925-065A-377541	Sequence 377541,
c 14	18.6	71.5	612	13	US-09-925-065A-377542	Sequence 377542,
c 15	18.6	71.5	612	13	US-09-925-065A-377543	Sequence 377543,
16	18.6	71.5	620	13	US-09-925-065A-414588	Sequence 414588,
17	18.6	71.5	620	13	US-09-925-065A-414589	Sequence 414589,
18	18.6	71.5	620	13	US-09-925-065A-414590	Sequence 414590,
19	18.6	71.5	1112	19	US-10-424-599-106760	Sequence 106760,
c 20	18.6	71.5	3112	26	US-11-097-143-8716	Sequence 8716, Ap
c 21	18.6	71.5	4331	26	US-11-097-143-8716	Sequence 8716, Ap
c 22	18.6	71.5	6426	26	US-11-097-143-8716	Sequence 8716, Ap
23	18.4	70.8	846	9	US-09-801-368-277	Sequence 277, App
24	18.4	70.8	846	18	US-10-369-493-25289	Sequence 25289, A
c 25	18.2	70.0	454	13	US-09-925-065A-96568	Sequence 96568, A
c 26	18.2	70.0	454	13	US-09-925-065A-96569	Sequence 96569, A
c 27	18.2	70.0	544	20	US-10-021-323-16363	Sequence 16363, A
c 28	18.2	70.0	553	13	US-09-925-065A-123177	Sequence 123177,
c 29	18.2	70.0	553	13	US-09-925-065A-123178	Sequence 123178,
c 30	18.2	70.0	553	13	US-09-925-065A-220655	Sequence 220655,
c 31	18.2	70.0	553	13	US-09-925-065A-220656	Sequence 220656,
c 32	18.2	70.0	581	13	US-09-925-065A-872784	Sequence 872784,
33	18.2	70.0	590	20	US-10-021-323-14869	Sequence 14869, A
34	18.2	70.0	617	9	US-09-974-300-1766	Sequence 1766, Ap
35	18.2	70.0	666	13	US-09-925-065A-677902	Sequence 677902,
36	18.2	70.0	814	20	US-10-767-795-5675	Sequence 5675, Ap
37	18.2	70.0	1011	18	US-10-369-493-35117	Sequence 35117, A
38	18.2	70.0	1011	18	US-10-369-493-38288	Sequence 38288, A
39	18.2	70.0	1011	18	US-10-369-493-38680	Sequence 38680, A
c 40	18.2	70.0	640681	9	US-09-790-988-1	Sequence 1, Appli
c 41	18	69.2	403	20	US-10-437-963-59536	Sequence 59536, A
c 42	18	69.2	600	24	US-10-972-079-48473	Sequence 48473, A
c 43	18	69.2	600	24	US-10-972-079-48474	Sequence 48474, A
c 44	18	69.2	612	13	US-09-925-065A-269722	Sequence 269722,
45	18	69.2	1075	13	US-09-925-065A-727798	Sequence 727798,

ALIGNMENTS

RESULT 1
US-10-025-137-8
; Sequence 8, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Terng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated probe
US-10-025-137-8

Query Match 100.0%; Score 26; DB 16; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 G T T A T G T A T T G C T G T T G C G G C G 26
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 519.22 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-7

Perfect score: 27

Sequence: 1 attttaccttcttctcccgctttgg 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	20.6	76.3	599	13	US-09-925-065A-745980
5	19.8	73.3	445	13	US-09-925-065A-290213

6	19.6	72.6	600	24	US-10-972-079-31542	Sequence 31542, A
7	19.6	72.6	600	24	US-10-972-079-31543	Sequence 31543, A
8	19.6	72.6	600	24	US-10-972-079-31544	Sequence 31544, A
9	19.6	72.6	600	24	US-10-972-079-31545	Sequence 31545, A
10	19.6	72.6	676	19	US-10-425-114-31270	Sequence 31270, A
11	19.6	72.6	676	21	US-10-425-115-134950	Sequence 134950, A
12	19.6	72.6	722	9	US-09-966-881-8	Sequence 8, Appli
13	19.6	72.6	730	19	US-10-425-114-5874	Sequence 5874, Ap
14	19.6	72.6	1293	19	US-10-425-114-31738	Sequence 31738, A
15	19.6	72.6	1318	21	US-10-425-115-134956	Sequence 134956, A
16	19.6	72.6	1334	21	US-10-425-115-134954	Sequence 134954, A
17	19.6	72.6	1460	19	US-10-425-114-34241	Sequence 34241, A
18	19.6	72.6	1460	21	US-10-425-115-134948	Sequence 134948, A
19	19	70.4	368	18	US-10-242-535A-40004	Sequence 40004, A
20	19	70.4	368	19	US-10-085-783A-40004	Sequence 40004, A
21	19	70.4	594	13	US-09-925-065A-932387	Sequence 932387, A
22	19	70.4	600	13	US-09-925-065A-932355	Sequence 932355, A
23	19	70.4	600	13	US-09-925-065A-932356	Sequence 932356, A
24	19	70.4	600	13	US-09-925-065A-932357	Sequence 932357, A
25	19	70.4	600	24	US-10-972-079-24595	Sequence 24595, A
26	19	70.4	1112	13	US-09-925-065A-283732	Sequence 283732, A
27	19	70.4	7372	24	US-10-073-735A-1	Sequence 1, Appli
28	18.6	68.9	453	13	US-09-925-065A-561153	Sequence 561153, A
29	18.6	68.9	482	14	US-10-027-632-188723	Sequence 188723, A
30	18.6	68.9	482	14	US-10-027-632-188724	Sequence 188724, A
31	18.6	68.9	482	18	US-10-027-632-188723	Sequence 188723, A
32	18.6	68.9	482	18	US-10-027-632-188724	Sequence 188724, A
33	18.6	68.9	573	13	US-09-925-065A-453195	Sequence 453195, A
34	18.6	68.9	589	13	US-09-925-065A-742966	Sequence 742966, A
35	18.6	68.9	589	13	US-09-925-065A-818082	Sequence 818082, A
36	18.6	68.9	624	13	US-09-925-065A-838563	Sequence 838563, A
37	18.6	68.9	624	13	US-09-925-065A-838564	Sequence 838564, A
38	18.6	68.9	657	13	US-09-925-065A-514497	Sequence 514497, A
39	18.6	68.9	1754	26	US-11-097-143-25148	Sequence 25148, A
40	18.6	68.9	2275	13	US-09-925-065A-686407	Sequence 686407, A
41	18.6	68.9	2275	13	US-09-925-065A-686408	Sequence 686408, A
42	18.6	68.9	2275	13	US-09-925-065A-686409	Sequence 686409, A
43	18.6	68.9	2275	13	US-09-925-065A-686410	Sequence 686410, A
44	18.6	68.9	2275	13	US-09-925-065A-686411	Sequence 686411, A
45	18.6	68.9	2275	13	US-09-925-065A-686412	Sequence 686412, A

ALIGNMENTS

RESULT 1

US-10-025-137-7

; Sequence 7: Application US/10025137

; Publication No. US20030113731A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Lu-Yieng

; APPLICANT: Chung, Te-Yu

; APPLICANT: Tserng, Harn-Jing

; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI

; FILE REFERENCE: 12674-005001

; CURRENT APPLICATION NUMBER: US/10/025,137

; CURRENT FILING DATE: 2001-12-19

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7

; LENGTH: 27

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetically generated probe

US-10-025-137-7

Query Match 100.0%; Score 27; DB 16; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTTTACCTTGTCTTCCCGCTTTGG 27
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 70.1152 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-7

Perfect score: 27

Sequence: 1 attttaccttcttctccgctcttg 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	19	70.4	451924	4	US-09-949-016-12896
4	19	70.4	451925	4	US-09-949-016-17305
5	18.6	68.9	7610	4	US-09-949-016-5516
6	18.6	68.9	7654	4	US-09-949-016-384
7	18.6	68.9	71645	4	US-09-949-016-12126
8	18.6	68.9	71651	4	US-09-949-016-17258
9	18.4	68.1	405	4	US-09-489-039A-4421
10	18	66.7	601	4	US-09-949-016-71161
11	18	66.7	601	4	US-09-949-016-164980
12	18	66.7	18888	4	US-09-949-016-16386
13	18	66.7	50950	4	US-09-949-016-16659
14	18	66.7	134008	4	US-09-949-016-13841
15	18	66.7	134140	4	US-09-949-016-12672
16	18	66.7	134241	4	US-09-949-016-12424
17	18	66.7	134242	4	US-09-949-016-15813
18	18	66.7	134242	4	US-09-949-016-15814
19	18	66.7	134242	4	US-09-949-016-15815
20	18	66.7	139552	4	US-09-949-016-15300
21	17.8	65.9	240	4	US-09-513-999C-31139
22	17.8	65.9	2373	4	US-09-543-681A-2288
23	17.6	65.2	558	3	US-08-930-285-17
24	17.6	65.2	601	4	US-09-949-016-37361
25	17.6	65.2	601	4	US-09-949-016-83346
26	17.6	65.2	601	4	US-09-949-016-144361
27	17.6	65.2	601	4	US-09-949-016-150418

C 28	17.6	65.2	601	4	US-09-949-016-150419	Sequence 150419, A
C 29	17.6	65.2	601	4	US-09-949-016-150420	Sequence 150420, A
C 30	17.6	65.2	601	4	US-09-949-016-196664	Sequence 196664, A
C 31	17.6	65.2	2625	4	US-09-949-016-4081	Sequence 4081, App
C 32	17.6	65.2	2640	4	US-09-949-016-994	Sequence 994, App
C 33	17.6	65.2	26852	4	US-09-949-016-12736	Sequence 12736, A
C 34	17.6	65.2	26852	4	US-09-949-016-15823	Sequence 15823, A
C 35	17.6	65.2	28585	4	US-09-949-016-17311	Sequence 17311, A
C 36	17.6	65.2	116652	4	US-09-949-016-13413	Sequence 13413, A
C 37	17.6	65.2	143550	4	US-09-949-016-14143	Sequence 14143, A
C 38	17.6	65.2	181251	4	US-09-949-016-15970	Sequence 15970, A
C 39	17.4	64.4	31144	4	US-09-949-016-15993	Sequence 15993, A
C 40	17.4	64.4	34658	4	US-09-949-016-12829	Sequence 12829, A
C 41	17.4	64.4	84495	3	US-09-797-906-3	Sequence 3, Appl
C 42	17.4	64.4	260247	4	US-09-949-016-13358	Sequence 13358, A
C 43	17.4	64.4	260286	4	US-09-949-016-17037	Sequence 17037, A
C 44	17.4	64.4	260293	4	US-09-949-016-12106	Sequence 12106, A
C 45	17.2	63.7	600	3	US-08-998-416-228	Sequence 228, App

ALIGNMENTS

RESULT 1
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; Sequence 13228, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13228
; LENGTH: 45249
; TYPE: DNA
; ORGANISM: Human
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Best Local Similarity 85.2%; Pred. No. 18;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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; Sequence 17078, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM nucleic - nucleic search, using sw model
Run on: November 4, 2005, 10:13:23 ; Search time 519.22 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-6
Perfect score: 27
Sequence: 1 aaacacctctctcgattctcac 27

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues 19589580

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
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- 22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
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- 24: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq.*
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- 28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 4	19.8	73.3	2681	19	US-10-467-042-26
C 5	19.8	73.3	2681	26	US-11-046-868-26

C 6	19.6	72.6	329	21	US-10-856-498-1702	Sequence 1702, Ap
C 7	19.6	72.6	348	21	US-10-856-499-1742	Sequence 1742, Ap
C 8	19.6	72.6	449	10	US-09-918-995-15975	Sequence 15975, A
C 9	19.2	71.1	6888	21	US-10-602-494-20	Sequence 20, Appl
C 10	19.2	71.1	6888	21	US-10-602-494-110	Sequence 110, Appl
C 11	19	70.4	1204	17	US-10-029-386-22637	Sequence 22637, A
C 12	19	70.4	2602	9	US-09-974-298-45	Sequence 45, Appl
C 13	19	70.4	9012	24	US-10-450-763-3921	Sequence 3921, Ap
C 14	19	70.4	9012	24	US-10-450-763-8552	Sequence 8552, Ap
C 15	19	70.4	9633	22	US-10-956-157-4420	Sequence 4420, Ap
C 16	19	70.4	10184	24	US-10-450-763-23875	Sequence 23875, A
C 17	18.8	69.6	33805	14	US-10-087-192-1483	Sequence 1483, Ap
C 18	18.6	68.9	201	21	US-10-719-993-19568	Sequence 19568, A
C 19	18.6	68.9	201	22	US-10-741-600-39403	Sequence 39403, A
C 20	18.6	68.9	580	13	US-09-925-065A-571437	Sequence 571437, A
C 21	18.6	68.9	626	13	US-09-925-065A-483342	Sequence 483342, A
C 22	18.6	68.9	638	20	US-10-767-701-8672	Sequence 8672, Ap
C 23	18.6	68.9	672	14	US-10-027-632-206505	Sequence 206505, A
C 24	18.6	68.9	672	14	US-10-027-632-206505	Sequence 206505, A
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C 26	18.6	68.9	1506	26	US-11-097-143-37523	Sequence 37523, A
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C 40	18.2	67.4	666	20	US-10-437-963-9460	Sequence 9460, Ap
C 41	18.2	67.4	681	13	US-09-925-065A-706860	Sequence 706860, A
C 42	18.2	67.4	681	13	US-09-925-065A-706861	Sequence 706861, A
C 43	18.2	67.4	829	15	US-10-198-846-3988	Sequence 3988, Ap
C 44	18.2	67.4	829	15	US-10-198-846-3988	Sequence 3988, Ap
C 45	18.2	67.4	1055	14	US-10-027-632-263005	Sequence 263005, A

ALIGNMENTS

RESULT 1
US-10-025-137-6
; Sequence 6, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025.137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated probe
US-10-025-137-6

Query Match 100.0%; Score 27; DB 16; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.019; 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0;

1 AAACACCTCTCTCGATTCTCAC 27
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 70.1152 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-6

Perfect score: 27

Sequence: 1 aaacacctctctctgagattcttcac 27

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	19.6	72.6	348	4	US-09-640-211A-1742
C 3	19.2	71.1	601	4	US-09-949-016-65388
C 4	19.2	71.1	45225	4	US-09-949-016-12428
C 5	19.2	71.1	45226	4	US-09-949-016-13654
C 6	19	70.4	1509	4	US-09-252-991A-5586
C 7	19	70.4	1524	4	US-09-252-991A-5643
C 8	18.6	68.9	2681	4	US-09-566-921-108
C 9	18.6	68.9	3528	1	US-08-286-889-36
C 10	18.6	68.9	3528	1	US-08-485-618-36
C 11	18.6	68.9	3528	1	US-08-362-652-36
C 12	18.6	68.9	3528	1	US-08-605-672-36
C 13	18.6	68.9	3528	2	US-08-482-293A-36
C 14	18.6	68.9	3528	2	US-08-943-363-36
C 15	18.6	68.9	3528	3	US-09-193-043-36
C 16	18.6	68.9	3528	3	US-09-688-307A-36
C 17	18.6	68.9	3528	4	US-09-350-259-36
C 18	18.6	68.9	3597	1	US-08-485-618-54
C 19	18.6	68.9	3597	1	US-08-362-652-54
C 20	18.6	68.9	3597	1	US-08-605-672-54
C 21	18.6	68.9	3597	2	US-08-482-293A-54
C 22	18.6	68.9	3597	2	US-08-943-363-54
C 23	18.6	68.9	3597	3	US-09-193-043-54
C 24	18.6	68.9	3597	3	US-09-688-307A-54
C 25	18.6	68.9	3597	4	US-09-350-259-54
C 26	18	66.7	1766	4	US-09-167-206-11
C 27	18	66.7	1845	4	US-09-949-016-1779

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c 28      18      66.7      1851      4      US-09-949-016-480      Sequence 480, App
29      18      66.7      78649      4      US-09-949-016-14619      Sequence 14619, A
30      18      66.7      78649      4      US-09-949-016-14620      Sequence 14620, A
31      18      66.7      78649      4      US-09-949-016-16227      Sequence 16227, A
32      18      66.7      78649      4      US-09-949-016-16228      Sequence 16228, A
33      18      66.7      83665      4      US-09-949-016-16995      Sequence 16995, A
34      18      66.7      221958      4      US-09-949-016-12173      Sequence 12173, A
35      18      66.7      221966      4      US-09-949-016-15498      Sequence 15498, A
36      17.6      65.2      601      4      US-09-949-016-38523      Sequence 38523, A
37      17.6      65.2      601      4      US-09-949-016-152047      Sequence 152047, A
38      17.6      65.2      601      4      US-09-949-016-152120      Sequence 152120, A
39      17.6      65.2      601      4      US-09-949-016-152193      Sequence 152193, A
40      17.6      65.2      601      4      US-09-949-016-152266      Sequence 152266, A
41      17.6      65.2      601      4      US-09-949-016-159352      Sequence 159352, A
42      17.6      65.2      601      4      US-09-949-016-159425      Sequence 159425, A
43      17.6      65.2      601      4      US-09-949-016-159498      Sequence 159498, A
44      17.6      65.2      601      4      US-09-949-016-159571      Sequence 159571, A
45      17.6      65.2      601      4      US-09-949-016-204129      Sequence 204129, A

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ALIGNMENTS

RESULT 1

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US-09-640-211A-1702/c
; Sequence 1702, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640.211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1702
; LENGTH: 329
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1702

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Query Match      72.6%; Score 19.6; DB 4; Length 329;
Best Local Similarity 84.6%; Pred. No. 17;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db      234      AAAACACCTCTTCTCGTCTTCTCTCA 209

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; Sequence 1742, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; APPLICANT: Glenn, Matthew
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640.211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1742
; LENGTH: 348
; TYPE: DNA

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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 519.22 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-5

Perfect score: 27

Sequence: 1 aatacataacagaacctgaacacaa 27

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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13: /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq.*

14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	21.2	78.5	731	18	Sequence 52, Appli
C 3	20.6	76.3	572	13	Sequence 472, App
C 4	20.6	76.3	572	13	Sequence 197203,
C 5	20.2	74.8	266	13	Sequence 197204,
					Sequence 18595, A

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6 20.2 74.8 550 13 US-09-925-065A-532578 Sequence 532578,
7 20.2 74.8 580 13 US-09-925-065A-374894 Sequence 374894,
8 20.2 74.8 616 13 US-09-925-065A-532579 Sequence 532579,
9 20.2 74.8 637 10 US-09-925-065A-532579 Sequence 58, Appl
c 10 20.2 74.8 643 13 US-09-925-065A-445185 Sequence 445185,
c 11 20.2 74.8 643 13 US-09-925-065A-445186 Sequence 445186,
c 12 20.2 74.8 643 13 US-09-925-065A-445187 Sequence 445187,
c 13 20.2 74.8 830 14 US-10-027-632-174075 Sequence 174075,
c 14 20.2 74.8 830 14 US-10-027-632-174075 Sequence 174075,
c 15 20.2 74.8 830 14 US-10-027-632-174075 Sequence 174075,
c 16 20.2 74.8 119472 22 US-10-741-600-176111 Sequence 17611, A
c 17 20.2 74.8 255015 22 US-10-741-600-176111 Sequence 953, App
c 18 20.2 74.8 854 19 US-10-425-114-953 Sequence 30589, A
c 19 20.2 74.8 919 21 US-10-425-114-953 Sequence 172, App
c 20 20.2 74.8 1282 21 US-10-739-330-172 Sequence 1247, App
c 21 20.2 74.8 6565 19 US-10-221-714A-187 Sequence 1247, App
c 22 20.2 74.8 7002 9 US-09-954-456-1247 Sequence 1247, App
c 23 20.2 74.8 7002 22 US-10-843-641A-4274 Sequence 4274, App
c 24 20.2 74.8 96592 11 US-09-997-722-88 Sequence 88, Appl
c 25 20.2 74.8 163350 22 US-10-469-052-3 Sequence 3, Appl
c 26 20.2 74.8 167343 9 US-09-962-436-281 Sequence 281, App
c 27 20.2 74.8 167343 9 US-09-964-824A-273 Sequence 273, App
c 28 20.2 74.8 167343 22 US-10-843-641A-2740 Sequence 2740, App
c 29 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 30 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 31 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 32 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 33 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 34 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 35 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 36 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 37 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 38 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 39 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 40 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 41 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 42 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 43 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
c 44 20.2 74.8 167343 22 US-10-843-641A-5576 Sequence 5576, App
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ALIGNMENTS

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US-10-025-137-5
; Sequence 5, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Teng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated probe
US-10-025-137-5
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Query Match 100.0%; Score 27; DB 16; Length 27;

Best Local Similarity 100.0%; Pred. No. 0.29;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATACATACAGAACCTGAACACAA 27

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 70.1152 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-5

Perfect score: 27

Sequence: 1 aatacataacagaacctgaacacaa 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	19.2	71.1	25190	4	US-09-949-016-15906
3	19.2	71.1	69263	4	US-09-949-016-12594
4	19.2	71.1	69709	4	US-09-949-016-16036
5	19.2	71.1	154915	4	US-09-949-016-15584
6	19	70.4	587	4	US-09-270-767-11712
7	19	70.4	601	4	US-09-949-016-147450
8	19	70.4	601	4	US-09-949-016-147451
9	19	70.4	77388	4	US-09-949-016-13496
10	19	70.4	78491	4	US-09-949-016-15132
11	19	70.4	87470	4	US-09-949-016-15881
12	19	70.4	107085	4	US-09-949-016-13157
13	19	70.4	115388	4	US-09-949-016-14981
14	19	70.4	127771	4	US-09-949-016-14982
15	19	70.4	253345	4	US-09-949-016-12656
16	19	70.4	253364	4	US-09-949-016-13639
17	18.6	68.9	112623	4	US-09-949-016-14374
18	18.2	67.4	1013	4	US-09-270-767-11613
19	18	66.7	451	4	US-09-679-409-49
20	18	66.7	601	4	US-09-949-016-69420
21	18	66.7	601	4	US-09-949-016-127473
22	18	66.7	601	4	US-09-949-016-195438
23	18	66.7	3001	4	US-09-539-333D-179
24	18	66.7	9098	4	US-09-358-082A-28
25	18	66.7	9098	4	US-09-358-082A-28
26	18	66.7	19296	4	US-09-949-016-16393
27	18	66.7	33731	4	US-09-949-016-13473

28	18	66.7	33731	4	US-09-949-016-13474	Sequence 13474, A
29	18	66.7	38814	4	US-09-949-016-13470	Sequence 13470, A
30	18	66.7	38814	4	US-09-949-016-13471	Sequence 13471, A
31	18	66.7	54649	4	US-09-949-016-15867	Sequence 15867, A
32	18	66.7	59319	4	US-09-949-016-16115	Sequence 16115, A
33	18	66.7	68436	4	US-09-949-016-12943	Sequence 12943, A
34	18	66.7	83428	4	US-09-949-016-13610	Sequence 13610, A
35	18	66.7	90472	4	US-09-949-016-14038	Sequence 14038, A
36	18	66.7	91665	4	US-09-949-016-12234	Sequence 12234, A
37	18	66.7	112132	3	US-09-741-150-3	Sequence 3, Appli
38	18	66.7	112132	4	US-10-160-187-3	Sequence 3, Appli
39	18	66.7	113100	4	US-09-949-016-12245	Sequence 12245, A
40	18	66.7	129327	4	US-09-949-016-12257	Sequence 12257, A
41	18	66.7	129327	4	US-09-949-016-15368	Sequence 15368, A
42	18	66.7	145241	4	US-09-949-016-17394	Sequence 17394, A
43	18	66.7	145241	4	US-09-949-016-17395	Sequence 17395, A
44	18	66.7	174639	4	US-09-949-016-16509	Sequence 16509, A
45	18	66.7	202001	4	US-09-734-674-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-949-016-12804
; Sequence 12804, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12804
; LENGTH: 64319
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12804

Query Match 73.3%; Score 19.8; DB 4; Length 64319;
Best Local Similarity 91.3%; Pred. No. 80;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 18750 ATAAATACAGAACTGAACA 18772

RESULT 2
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; Sequence 15906, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR APPLICATION NUMBER: 60/231,498

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-4

Perfect score: 24
Sequence: 1 acgccgttaggtgattgtg 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 23: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 27: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	24	100.0	4402	US-10-450-763-25521	Sequence 25521, A
3	18	75.0	18	US-10-025-137-2	Sequence 2, Appli
4	17.2	71.7	225	US-10-724-972A-1325	Sequence 1325, Ap
5	17	70.8	25	US-10-719-900-455085	Sequence 455085,

6	17	70.8	501	13	US-09-925-065A-816484	Sequence 816484,
7	16.8	70.0	611	13	US-09-925-065A-747394	Sequence 747394,
8	16.8	70.0	620	13	US-09-925-065A-735148	Sequence 735148,
9	16.8	70.0	1545	9	US-09-815-243-4756	Sequence 4756, Ap
10	16.8	70.0	1578	9	US-09-815-243-8828	Sequence 8828, Ap
11	16.8	70.0	1578	18	US-10-282-132A-7945	Sequence 7945, Ap
12	16.8	70.0	3730	24	US-10-795-159-481	Sequence 481, App
13	16.8	70.0	18355	8	US-08-781-986A-67	Sequence 67, Appl
14	16.8	70.0	18355	22	US-10-329-624-67	Sequence 17808, A
15	16.8	70.0	28724	19	US-10-741-600-17808	Sequence 17808, A
16	16.8	70.0	36714	20	US-10-322-281-864	Sequence 864, App
17	16.8	70.0	60989	18	US-10-292-798-197	Sequence 197, App
18	16.8	70.0	417576	24	US-10-795-159-684	Sequence 684, App
19	16.8	70.0	1830121	18	US-10-329-670-1	Sequence 1, Appli
20	16.8	70.0	1830121	21	US-10-158-865-1	Sequence 1, Appli
21	16.8	70.0	1830121	24	US-10-981-687-1	Sequence 1, Appli
22	16.6	69.2	240	21	US-10-425-115-155871	Sequence 155871,
23	16.6	69.2	509	9	US-09-864-761-7520	Sequence 7520, Ap
24	16.6	69.2	509	17	US-10-029-386-3390	Sequence 3390, Ap
25	16.6	69.2	839	21	US-10-363-345A-15251	Sequence 15251, A
26	16.6	69.2	839	21	US-10-363-345A-15252	Sequence 15252, A
27	16.6	69.2	839	22	US-10-363-483A-15251	Sequence 15251, A
28	16.6	69.2	839	22	US-10-363-483A-15252	Sequence 15252, A
29	16.6	69.2	2724	24	US-10-450-763-10761	Sequence 10761, A
30	16.6	69.2	2729	24	US-10-450-763-21785	Sequence 21785, A
31	16.6	69.2	27681	9	US-09-764-869-1997	Sequence 1997, Ap
32	16.6	69.2	27681	9	US-09-764-869-1998	Sequence 1998, Ap
33	16.6	69.2	27681	15	US-10-091-504-1997	Sequence 1997, Ap
34	16.6	69.2	27681	15	US-10-091-504-1998	Sequence 1998, Ap
35	16.6	69.2	27681	18	US-10-227-577-1997	Sequence 1997, Ap
36	16.6	69.2	27681	18	US-10-227-577-1998	Sequence 1998, Ap
37	16.6	69.2	86114	16	US-10-080-170-648	Sequence 648, App
38	16.6	69.2	86114	20	US-10-080-170-648	Sequence 648, App
39	16.6	69.2	86114	20	US-10-468-356-648	Sequence 648, App
40	16.6	69.2	243390	20	US-10-322-281-462	Sequence 462, App
41	16.6	69.2	1830121	18	US-10-329-670-1	Sequence 1, Appli
42	16.6	69.2	1830121	21	US-10-158-865-1	Sequence 1, Appli
43	16.6	69.2	1830121	24	US-10-981-687-1	Sequence 1, Appli
44	16.4	68.3	583	13	US-09-925-065A-818153	Sequence 818153,
45	16.4	68.3	583	13	US-09-925-065A-841207	Sequence 841207,

ALIGNMENTS

RESULT 1
US-10-025-137-4
; Sequence 4, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Tserng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-10-025-137-4

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Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGCCGTtaggtgattgtg 24
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 62.3246 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-4
Perfect score: 24
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Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	17.2	71.7	3005	4	US-09-710-279-3452
5	17.2	71.7	3065	4	US-09-710-279-3697
6	17.2	71.7	3172	4	US-09-710-279-3876
7	17.2	71.7	3172	4	US-09-710-279-4314
8	16.8	70.0	18355	4	US-08-956-171E-67
9	16.8	70.0	18355	4	US-08-781-986A-67
10	16.8	70.0	1830121	4	US-09-557-884-1
11	16.8	70.0	1830121	4	US-09-643-990A-1
12	16.6	69.2	227390	4	US-09-949-016-12201
13	16.6	69.2	227391	4	US-09-949-016-13365
14	16.6	69.2	1830121	4	US-09-557-884-1
15	16.6	69.2	1830121	4	US-09-643-990A-1
16	16.6	69.2	4403765	3	US-09-103-840A-2
17	16.6	69.2	4411529	3	US-09-103-840A-1
18	16.4	68.3	10783	4	US-09-949-016-16290
19	16.2	67.5	601	4	US-09-949-016-14180
20	16.2	67.5	2871	4	US-09-949-016-3998
21	16.2	67.5	3650	4	US-09-620-312D-30
22	16.2	67.5	29433	4	US-09-949-016-15740
23	16.2	67.5	1664376	4	US-08-916-421B-1
24	16.2	67.5	1664976	4	US-09-692-570-1
25	16	66.7	2613	3	US-09-221-017B-563
26	16	66.7	219944	4	US-09-949-016-15086
27	16	66.7	1664976	4	US-08-916-421B-1

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		15.8	65.8	309	4	US-09-134-000C-272	Sequence 272, App
c	30	15.8	65.8	601	4	US-09-949-016-142400	Sequence 142400,
c	31	15.8	65.8	601	4	US-09-949-016-167522	Sequence 167522,
c	32	15.8	65.8	39433	4	US-09-949-016-12014	Sequence 12014, A
c	33	15.8	65.8	58133	4	US-09-949-016-16464	Sequence 16464, A
c	34	15.8	65.8	96340	4	US-09-949-016-15863	Sequence 15863, A
c	35	15.8	65.8	211049	4	US-09-949-016-15770	Sequence 15770, A
c	36	15.6	65.0	390	4	US-09-489-039A-4446	Sequence 4446, Ap
c	37	15.6	65.0	501	4	US-09-489-039A-4467	Sequence 4467, Ap
c	38	15.6	65.0	526	4	US-08-956-171E-1135	Sequence 1135, Ap
c	39	15.6	65.0	526	4	US-08-781-986A-1135	Sequence 1135, Ap
c	40	15.6	65.0	756	4	US-09-134-000C-1161	Sequence 1161, Ap
c	41	15.6	65.0	1386	4	US-09-248-796A-4123	Sequence 4123, Ap
c	42	15.6	65.0	7278	3	US-09-091-219-1	Sequence 1, Appli
c	43	15.6	65.0	7278	4	US-09-660-541-1	Sequence 1, Appli
c	44	15.6	65.0	19412	4	US-09-949-016-17094	Sequence 17094, A
c	45	15.6	65.0	53336	4	US-09-949-016-12500	Sequence 12500, A

ALIGNMENTS

RESULT 1
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; Sequence 166018, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166018
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-166018

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Best Local Similarity 83.3%; Pred. No. 46;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 464 ATGCCGTTGGTGTATTGATGTG 487

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; Sequence 16420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 461.529 Seconds
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430.040 Million cell updates/sec

Title: US-10-025-137B-3
Perfect score: 24
Sequence: 1 tgaatgcgaagctgaaaagtag 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	18.2	75.8	600	US-10-972-079-81835	Sequence 81835, A
3	18.2	75.8	609	US-09-525-065A-481749	Sequence 481749, A
4	18.2	75.8	1224	US-11-097-143-31046	Sequence 31046, A
5	18.2	75.8	3224	US-11-097-143-31045	Sequence 31045, A

6	18	75.0	18	US-10-025-137-1	Sequence 1, Appli
7	17.8	74.2	204	US-10-437-963-80131	Sequence 80131, A
8	17.8	74.2	700	US-10-027-632-149388	Sequence 149388, A
9	17.8	74.2	700	US-10-027-632-149388	Sequence 149388, A
10	17.8	74.2	1221	US-10-369-493-47169	Sequence 47169, A
11	17.8	74.2	1482	US-09-070-927A-842	Sequence 842, App
12	17.8	74.2	2658	US-09-227-742-14	Sequence 14, Appl
13	17.8	74.2	2658	US-10-901-199-14	Sequence 14, Appl
14	17.6	73.3	550	US-10-663-561-310	Sequence 310, App
15	17.6	73.3	554	US-10-027-632-271125	Sequence 271125, A
16	17.6	73.3	554	US-10-027-632-271125	Sequence 271125, A
17	17.6	73.3	581	US-09-925-065A-311952	Sequence 311952, A
18	17.6	73.3	919	US-09-815-242-2910	Sequence 2910, Ap
19	17.6	73.3	919	US-10-282-122A-5489	Sequence 5489, Ap
20	17.6	73.3	972	US-10-109-310-22	Sequence 22, Appl
21	17.6	73.3	1006	US-08-781-986A-386	Sequence 386, App
22	17.6	73.3	1006	US-10-329-624-386	Sequence 386, App
23	17.6	73.3	1170	US-10-437-963-23358	Sequence 23358, A
24	17.6	73.3	1260	US-09-925-065A-674296	Sequence 674296, A
25	17.6	73.3	1458	US-09-815-242-4375	Sequence 4375, Ap
26	17.6	73.3	1470	US-10-282-122A-8209	Sequence 8209, Ap
27	17.6	73.3	1470	US-10-857-625-423	Sequence 423, App
28	17.6	73.3	1515	US-09-815-242-8388	Sequence 8388, Ap
29	17.6	73.3	1603	US-10-437-963-50038	Sequence 50038, A
30	17.6	73.3	2238	US-10-027-632-260220	Sequence 260220, A
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40	17.6	73.3	47804	US-10-017-161-717	Sequence 717, App
41	17.6	73.3	47804	US-10-292-798-629	Sequence 629, App
42	17.6	73.3	107304	US-10-322-281-249	Sequence 249, App
43	17.6	73.3	335913	US-09-754-853A-2	Sequence 2, Appli
44	17.6	73.3	335913	US-09-754-853A-3	Sequence 3, Appli
45	17.6	73.3	392000	US-10-027-983-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-10-025-137-3
; Sequence 3, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Tsering, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-10-025-137-3

Query Match 100.0%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAATGCGCAAGCTGAAAAGTAG 24
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 62.3246 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-3
Perfect score: 24
Sequence: 1 tgaatgcgaagctgaaaaagtag 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.8	74.2	2658	2	US-08-826-426-14
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3	17.6	73.3	972	3	US-09-215-694-22
4	17.6	73.3	1006	4	US-08-956-171E-386
5	17.6	73.3	1006	4	US-08-781-986A-386
6	17.6	73.3	1101	4	US-09-328-352-1336
7	17.6	73.3	1888	3	US-08-737-226-3
8	17.6	73.3	2525	3	US-08-714-918-84
9	17.6	73.3	2525	3	US-09-265-315-84
10	17.6	73.3	2525	3	US-09-265-315-84
11	17.6	73.3	2525	3	US-09-266-417-84
12	17.6	73.3	2525	4	US-09-528-709-84
13	17.6	73.3	2525	4	US-09-527-745-84
14	17.6	73.3	10088	4	US-08-956-171E-32
15	17.6	73.3	10088	4	US-08-781-986A-32
16	17.6	73.3	33000	3	US-09-215-694-18
17	17.6	73.3	325034	4	US-09-949-016-14957
18	17.6	73.3	389504	4	US-09-949-016-11774
19	17.6	73.3	392000	4	US-10-027-983-11
20	17.2	71.7	163	4	US-09-513-999C-33278
21	17.2	71.7	396	4	US-09-583-110-234
22	17.2	71.7	897	4	US-09-270-767-3490
23	17.2	71.7	897	4	US-09-270-767-18772
24	17.2	71.7	1908	4	US-09-543-681A-1784
25	17.2	71.7	11378	3	US-08-961-527-210
26	16.8	70.0	777	4	US-09-328-352-4023
27	16.8	70.0	142783	4	US-09-949-016-15127

28	16.8	70.0	818128	4	US-09-949-016-14546	Sequence 14546, A
29	16.8	70.0	818128	4	US-09-949-016-14547	Sequence 14547, A
30	16.8	70.0	818128	4	US-09-949-016-14548	Sequence 14548, A
31	16.8	70.0	818128	4	US-09-949-016-14549	Sequence 14549, A
32	16.8	70.0	818128	4	US-09-949-016-14550	Sequence 14550, A
33	16.8	70.0	818128	4	US-09-949-016-14551	Sequence 14551, A
34	16.8	70.0	818128	4	US-09-949-016-14552	Sequence 14552, A
35	16.8	70.0	818128	4	US-09-949-016-14553	Sequence 14553, A
36	16.8	70.0	818128	4	US-09-949-016-14554	Sequence 14554, A
37	16.8	70.0	818128	4	US-09-949-016-14555	Sequence 14555, A
38	16.8	70.0	818128	4	US-09-949-016-14556	Sequence 14556, A
39	16.8	70.0	818128	4	US-09-949-016-14557	Sequence 14557, A
40	16.8	70.0	818128	4	US-09-949-016-14558	Sequence 14558, A
41	16.8	70.0	818128	4	US-09-949-016-14559	Sequence 14559, A
42	16.8	70.0	818128	4	US-09-949-016-14560	Sequence 14560, A
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44	16.8	70.0	818128	4	US-09-949-016-14562	Sequence 14562, A
45	16.8	70.0	818128	4	US-09-949-016-14564	Sequence 14564, A

ALIGNMENTS

RESULT 1
US-08-826-426-14
; Sequence 14, Application US/08826426
; Patent No. 5891692
; GENERAL INFORMATION:
; APPLICANT: BLOOM, FREDERIC
; APPLICANT: KUO, JONATHAN
; APPLICANT: LIN, JHY-JHU
; APPLICANT: MA, JIN
; TITLE OF INVENTION: METHOD FOR INCREASING VIABILITY
; TITLE OF INVENTION: AND TRANSFORMATION EFFICIENCY OF BACTERIA DURING
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/826,426
APPLICATION NUMBER: US/08/826,426
FILING DATE: 27-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Ser. No. 5891692 60/014,330
FILING DATE: 29-MAR-1996
APPLICATION NUMBER: U.S. Ser. No. 5891692 60/025,838
FILING DATE: 05-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Auerbach, Jeffrey
REGISTRATION NUMBER: 32,680
REFERENCE/DOCKET NUMBER: 04227-0031
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 383-7451
TELEFAX: 202 383-6610
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2658 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-826-426-14

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 346.147 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-2

Perfect score: 18

Sequence: 1 ttagggtattgttg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	16	88.9	501	13	US-09-925-065A-816484

c 6	15.4	85.6	497	13	US-09-925-065A-182186	Sequence 182186,
c 7	15.4	85.6	497	13	US-09-925-065A-182187	Sequence 182187,
c 8	15.4	85.6	522	17	US-10-029-386-5126	Sequence 5126, Ap
c 9	15.4	85.6	537	14	US-10-027-632-186868	Sequence 186868,
c 10	15.4	85.6	537	18	US-10-027-632-186868	Sequence 186868,
c 11	15.4	85.6	534	13	US-09-925-065A-406303	Sequence 406303,
c 12	15.4	85.6	572	14	US-10-027-632-225990	Sequence 225990,
c 13	15.4	85.6	572	18	US-10-027-632-225990	Sequence 225990,
c 14	15.4	85.6	583	13	US-09-925-065A-818153	Sequence 818153,
c 15	15.4	85.6	583	13	US-09-925-065A-841207	Sequence 841207,
c 16	15.4	85.6	604	14	US-10-027-632-212524	Sequence 212524,
c 17	15.4	85.6	604	18	US-10-027-632-212524	Sequence 212524,
c 18	15.4	85.6	611	13	US-09-925-065A-747394	Sequence 747394,
c 19	15.4	85.6	618	13	US-09-925-065A-246000	Sequence 246000,
c 20	15.4	85.6	620	13	US-09-925-065A-735148	Sequence 735148,
c 21	15.4	85.6	656	13	US-09-925-065A-415746	Sequence 415746,
c 22	15.4	85.6	820	14	US-10-027-632-173633	Sequence 173633,
c 23	15.4	85.6	820	14	US-10-027-632-173634	Sequence 173634,
c 24	15.4	85.6	820	18	US-10-027-632-173633	Sequence 173633,
c 25	15.4	85.6	820	18	US-10-027-632-173634	Sequence 173634,
c 26	15.4	85.6	1214	14	US-10-027-632-212523	Sequence 212523,
c 27	15.4	85.6	1214	18	US-10-027-632-212523	Sequence 212523,
c 28	15.4	85.6	1545	9	US-09-815-242-4756	Sequence 4756, Ap
c 29	15.4	85.6	1578	9	US-09-815-242-8828	Sequence 8828, Ap
c 30	15.4	85.6	3129	18	US-10-282-122A-7945	Sequence 7945, Ap
c 31	15.4	85.6	3129	18	US-10-282-122A-11102	Sequence 11102, A
c 32	15.4	85.6	3540	18	US-10-282-122A-24459	Sequence 24459, A
c 33	15.4	85.6	4053	9	US-09-070-927A-407	Sequence 407, App
c 34	15.4	85.6	5185	16	US-10-311-455-1008	Sequence 1008, Ap
c 35	15.4	85.6	5518	16	US-10-240-453-180	Sequence 180, App
c 36	15.4	85.6	6624	16	US-10-311-455-16	Sequence 16, Appl
c 37	15.4	85.6	7168	19	US-10-240-589C-39	Sequence 39, Appl
c 38	15.4	85.6	12138	16	US-10-311-455-1601	Sequence 1601, Ap
c 39	15.4	85.6	12138	18	US-10-257-166-115	Sequence 115, App
c 40	15.4	85.6	17280	19	US-10-221-714A-497	Sequence 497, App
c 41	15.4	85.6	18355	8	US-08-781-986A-67	Sequence 67, Appl
c 42	15.4	85.6	61020	19	US-10-329-624-67	Sequence 67, Appl
c 43	15.4	85.6	61020	19	US-10-221-714A-514	Sequence 514, App
c 44	15	83.3	465	14	US-10-027-632-83432	Sequence 83432, A
c 45	15	83.3	465	14	US-10-027-632-83433	Sequence 83433, A

ALIGNMENTS

RESULT 1
US-10-025-137-2
; Sequence 2, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Tserng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-10-025-137-2

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred.No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGTGATTGTTG 18
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 46.7435 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-2

Perfect score: 18
Sequence: 1 ttagggtattgattgtg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:
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4: /cgn2_6/ptodata/1/ina/5B_COMB.seq:
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	10783	4	US-09-949-016-16290 Sequence 16290, A
2	15.4	85.6	309	4	US-09-134-000C-272 Sequence 272, App
3	15.4	85.6	1386	4	US-09-248-796A-4123 Sequence 4123, Ap
4	15.4	85.6	1800	4	US-09-248-796A-4214 Sequence 4214, Ap
5	15.4	85.6	18355	4	US-08-956-171E-67 Sequence 67, Appl
6	15.4	85.6	18355	4	US-08-781-986A-67 Sequence 67, Appl
7	15	83.3	1596	3	US-09-134-001C-737 Sequence 737, App
8	15	83.3	236341	4	US-09-949-016-13978 Sequence 13978, A
9	14.8	82.2	390	4	US-09-489-039A-4446 Sequence 4446, App
10	14.8	82.2	457	4	US-09-621-976-130 Sequence 130, App
11	14.8	82.2	496	3	US-09-036-574-6 Sequence 6, Appli
12	14.8	82.2	496	4	US-08-454-294A-6 Sequence 6, Appli
13	14.8	82.2	501	4	US-09-489-039A-4467 Sequence 4467, Ap
14	14.8	82.2	601	4	US-09-949-016-142400 Sequence 142400,
15	14.8	82.2	601	4	US-09-949-016-166018 Sequence 166018,
16	14.8	82.2	601	4	US-09-949-016-167522 Sequence 167522,
17	14.8	82.2	1132	3	US-09-036-574-8 Sequence 8, Appli
18	14.8	82.2	1132	4	US-08-454-294A-8 Sequence 8, Appli
19	14.8	82.2	1137	4	US-09-248-796A-151 Sequence 151, App
20	14.8	82.2	1703	4	US-09-057-996-3 Sequence 3, Appli
21	14.8	82.2	6091	3	US-09-453-702B-200 Sequence 200, App
22	14.8	82.2	15402	4	US-09-949-016-12868 Sequence 12868, A
23	14.8	82.2	17842	4	US-09-949-016-13826 Sequence 13826, A
24	14.8	82.2	24000	4	US-09-949-016-14421 Sequence 14421, A
25	14.8	82.2	39433	4	US-09-949-016-12014 Sequence 12014, A
26	14.8	82.2	42075	4	US-09-949-016-14995 Sequence 14995, A
27	14.8	82.2	58133	4	US-09-949-016-16464 Sequence 16464, A

28	14.8	82.2	88906	4	US-09-949-016-17468 Sequence 17468, A
29	14.8	82.2	96340	4	US-09-949-016-15863 Sequence 15863, A
30	14.8	82.2	139552	4	US-09-949-016-15300 Sequence 15300, A
31	14.8	82.2	211049	4	US-09-949-016-15770 Sequence 15770, A
32	14.8	82.2	234884	4	US-09-949-016-16420 Sequence 16420, A
33	14.8	82.2	253345	4	US-09-949-016-12656 Sequence 12656, A
34	14.8	82.2	253364	4	US-09-949-016-13639 Sequence 13639, A
35	14.8	82.2	340380	4	US-09-949-016-14179 Sequence 14179, A
36	14.8	82.2	1664976	4	US-08-916-421B-1 Sequence 1, Appli
37	14.8	82.2	1664976	4	US-09-692-570-1 Sequence 7582, Ap
38	14.4	80.0	204	4	US-09-248-796A-121 Sequence 121, App
39	14.4	80.0	234	4	US-09-495-050A-121 Sequence 121, App
40	14.4	80.0	360	4	US-09-248-796A-7584 Sequence 7584, Ap
41	14.4	80.0	543	4	US-09-134-000C-2288 Sequence 2288, Ap
42	14.4	80.0	603	4	US-09-540-236-607 Sequence 607, App
43	14.4	80.0	1101	4	US-09-543-681A-3334 Sequence 3334, Ap
44	14.4	80.0	1347	4	US-09-134-000C-479 Sequence 479, App
45	14.4	80.0	3282	4	US-09-511-881A-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-16290
; Sequence 16290, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16290
; LENGTH: 10783
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16290

Query Match 91.1% Score 16.4; DB 4; Length 10783;
Best Local Similarity 94.4% Pred. NO. 90;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTAGGTGATTGATTGTG 18
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Db 4089 TTAGTGTATTGATTGTG 4106

RESULT 2
US-09-134-000C-272
; Sequence 272, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 272